

Claim 4. (Amended) A human SMN gene according to Claim 3, which comprises the following intronic sequences:

-for intron n° 6 SEQ ID NO:1:

[5' AATTTTAAATTTTTGTAGAGACAGGGTCTCATTATGTTGCCAGGGTG  
GTGTCAAGCTCCAGGTCTCAAGTGATCCCCCTACCTCCGCCTCCCAAAGTTGT  
GGGATTGTAGGCATGAGCCACTGCAAGAAAACCTTAAGTGCAGCCTAATAATT  
GTTTTCTTTGGGATAACTTTTAAAGTACATTAAAAGACTATCAACTTAATTTT  
TGATCATATTTTGTGAATAAAATAAGTAAAATGTCTTGTGAACAAAATGCTT  
TTTAACATCCATATAAAGCTATCTATATATAGCTATCTATGTCTATATAGCTA  
TTTTTTTAACTTCCTTTTATTTCCTTACAG 3']

-for intron n° 7 SEQ ID NO:2:

[5' GTAAGTCTGCCAGCATTATGAAAGTGAATCTTACTTTTGTAACCTTTAT  
GGTTTGTGGAAAACAAATGTTTTTGAACAGTTAAAAAGTTCAGATGTTAAAA  
GTTGAAAGGTTAATGTAAAACAATCAATATTAAAGAATTTTGATGCCAAACT  
ATTAGATAAAAGGTTAATCTACATCCCTACTAGAATTCTCATACTTAACTGGT  
TGGTTATGTGGAAGAAACATACTTTCACAATAAAGAGCTTTAGGATATGATGC  
CATTTTATATCACTAGTAGGCAGACCAGCAGACTTTTTTTTATTGTGATATGG  
GATAACCTAGGCATACTGCACTGTACACTCTGACATATGAAGTGCTCCTAGTCA  
AGTTTAACTGGTGTCCACAGAGGACATGGTTTAACTGGAATTCGTCAAGCCTC  
TGTTTCTAATTTCTCATTGTCAG 3'].

Claim 10, line 2, change "Claim 3" to --cDNA sequence of  
Fig. 3--;  
change "in stringents" to --under stringent-  
-;

line 3, change "Claims 1 to 9" to --Claims 3 to 9--.

Claim 14. (Amended) An isolated nucleotide sequence selected among the following sequences:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6)

5' GTAATAACCAAATGCAATGTGAA 3' (SEQ ID NO:7)

5' CTACAACACCCTTCTCACAG 3' (SEQ ID NO:8)

Claim 15. (Amended) A set of primers comprising:

-a pair of primers contained in the sequence comprising nucleotides 921 to 1469 of the sequence of Figure 3 and/or

-a pair of primers comprising the following sequences:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6).

Claim 16. (Amended) A set of primers selected from the group consisting of:

5' AGACTATCAACTTAATTTCTGATCA 3' (SEQ ID NO:5)

5' TAAGGAATGTGAGCACCTTCCTTC 3' (SEQ ID NO:6)

5' GTAATAACCAAATGCAATGTGAA 3' (SEQ ID NO:7)

5' CTACAACACCCTTCTCACAG 3' (SEQ ID NO:8)

5' AGG GCG AGG CTC TGT CTC A 3' (SEQ ID NO:24)

5' CGG GAG GAC CGC TTG TAG T 3' (SEQ ID NO:25);

5' GCC GGA AGT CGT CAC TCT T 3' (SEQ ID NO:26)

5' GGG TGC TGA GAG CGC TAA TA 3' (SEQ ID NO:27);

5' TGT GTG GAT TAA GAT GAC TC 3' (SEQ ID NO:28)  
5' CAC TTT ATC GTA TGT TAT C 3' (SEQ ID NO:29);  
5' CTG TGC ACC ACC CTG TAA CAT G 3' (SEQ ID NO:30)  
5' AAG GAC TAA TGA GAC ATC C 3' (SEQ ID NO:31);  
5' CGA GAT GAT AGT TTG CCC TC 3' (SEQ ID NO:32)  
5' AG CTA CTT CAC AGA TTG GGG AAA G 3' (SEQ ID NO:33);  
5' CTC ATC TAG TCT CTG CTT CC 3' (SEQ ID NO:34)  
5' TGG ATA TGG AAA TAG AGA GGG AGC 3' (SEQ ID NO:35);  
5' CAC CCT TAT AAC AAA AAC CTG C 3' (SEQ ID NO:36)  
5' GAG AAA GGA GTT CCA TGG AGC AG 3' (SEQ ID NO:37);  
5' GAG AGG TTA AAT GTC CCG AC 3' (SEQ ID NO:38)  
5' GTG AGA ACT CCA GGT CTC CTG G 3' (SEQ ID NO:39);  
5' TGA GTC TGT TTG ACT TCA GG 3' (SEQ ID NO:40)  
5' GAA GGA AAT GGA GGC AGC CAG C 3' (SEQ ID NO:41);  
5' TTT CTA CCC ATT AGA ATC TGG 3' (SEQ ID NO:42)  
5' CCC CAC TTA CTA TCA TGC TGG CTG 3' (SEQ ID NO:43);  
5' CCA GAC TTT ACT TTT TGT TTA CTG 3' (SEQ ID NO:44)  
5' ATA GCC ACT CAT GTA CCA TGA 3' (SEQ ID NO:45);  
5' AAG AGT AAT TTA AGC CTC AGA CAG 3' (SEQ ID NO:46)  
5' CTC CCA TAT GTC CAG ATT CTC TTG 3' (SEQ ID NO:47);  
5' AGA CTA TCA ACT TAA TTT CTG ATC A 3' (SEQ ID NO:48)  
5' TAA GGA ATG TGA GCA CCT TCC TTC 3' (SEQ ID NO:49);  
5' AGA CTA TCA ACT TAA TTT CTG ATC A 3' (SEQ ID NO:50)  
5' GTA AGA TTC ACT TTC ATA ATG CTG 3' (SEQ ID NO:51);  
5' CTT TAT GGT TTG TGG AAA ACA 3' (SEQ ID NO:52)  
5' GGC ATC ATA TCC TAA AGC TC 3' (SEQ ID NO:53);

[5' CGA GAT GAT AGT TTG CCC TC 3'  
 5' AG CTA CTT CAC AGA TTG GGG AAA G 3';  
 5' CTC ATC TAG TGT CTG CTT CC 3'  
 5' TGG ATA TGG AAA TAG AGA GGG AGC 3';  
 5' CAC CCT TAT AAC AAA AAC CTG C 3'  
 5' GAG AAA GGA GTT CCA TGG AGC AG 3';  
 5' GAG AGG TTA AAT GTC CCG AC 3'  
 5' GTG AGA ACT CCA GGT CTC CTG G 3';  
 5' TGA GTC TGT TTG ACT TCA GG 3'  
 5' GAA GGA AAT GGA GGC AGC CAG C 3';  
 5' TTT CTA CCC ATT AGA ATC TGG 3'  
 5' CCC CAC TTA CTA TCA TGC TGG CTG 3';  
 5' CCA GAC TTT ACT TTT TGT TTA CTG 3'  
 5' ATA GCC ACT CAT GTA CCA TGA 3';  
 5' AAG AGT AAT TTA AGC CTC AGA CAG 3'  
 5' CTC CCA TAT GTC CAG ATT CTC TTG 3';  
 5' AGA CTA TCA ACT TAA TTT CTG ATC A 3'  
 5' TAA GGA ATG TGA GCA CCT TCC TTC 3';  
 5' AGA CTA TCA ACT TAA TTT CTG ATC A 3'  
 5' GTA AGA TTC ACT TTC ATA ATG CTG 3';  
 5' CTT TAT GGT TTG TGG AAA ACA 3'  
 5' GGC ATC ATA TCC TAA AGC TC 3';]  
 5' GTA ATA ACC AAA TGC AAT GTG AA 3' (SEQ ID NO:54)  
 5' CTA CAA CAC CCT TCT CAC AG 3' (SEQ ID NO:55); and  
 5' GGT GTC CAC AGA GGA CAT GG 3' (SEQ ID NO:56)  
 5' AAG AGT TAA CCC ATT CCA GCT TCC 3' (SEQ ID NO:57).

5' 2' 3' 4' 5' 6' 7' 8' 9' 10' 11' 12' 13' 14' 15' 16' 17' 18' 19' 20' 21' 22' 23' 24' 25' 26' 27' 28' 29' 30' 31' 32' 33' 34' 35' 36' 37' 38' 39' 40' 41' 42' 43' 44' 45' 46' 47' 48' 49' 50' 51' 52' 53' 54' 55' 56' 57' 58' 59' 60' 61' 62' 63' 64' 65' 66' 67' 68' 69' 70' 71' 72' 73' 74' 75' 76' 77' 78' 79' 80' 81' 82' 83' 84' 85' 86' 87' 88' 89' 90' 91' 92' 93' 94' 95' 96' 97' 98' 99' 100' 101' 102' 103' 104' 105' 106' 107' 108' 109' 110' 111' 112' 113' 114' 115' 116' 117' 118' 119' 120' 121' 122' 123' 124' 125' 126' 127' 128' 129' 130' 131' 132' 133' 134' 135' 136' 137' 138' 139' 140' 141' 142' 143' 144' 145' 146' 147' 148' 149' 150' 151' 152' 153' 154' 155' 156' 157' 158' 159' 160' 161' 162' 163' 164' 165' 166' 167' 168' 169' 170' 171' 172' 173' 174' 175' 176' 177' 178' 179' 180' 181' 182' 183' 184' 185' 186' 187' 188' 189' 190' 191' 192' 193' 194' 195' 196' 197' 198' 199' 200' 201' 202' 203' 204' 205' 206' 207' 208' 209' 210' 211' 212' 213' 214' 215' 216' 217' 218' 219' 220' 221' 222' 223' 224' 225' 226' 227' 228' 229' 230' 231' 232' 233' 234' 235' 236' 237' 238' 239' 240' 241' 242' 243' 244' 245' 246' 247' 248' 249' 250' 251' 252' 253' 254' 255' 256' 257' 258' 259' 260' 261' 262' 263' 264' 265' 266' 267' 268' 269' 270' 271' 272' 273' 274' 275' 276' 277' 278' 279' 280' 281' 282' 283' 284' 285' 286' 287' 288' 289' 290' 291' 292' 293' 294' 295' 296' 297' 298' 299' 300' 301' 302' 303' 304' 305' 306' 307' 308' 309' 310' 311' 312' 313' 314' 315' 316' 317' 318' 319' 320' 321' 322' 323' 324' 325' 326' 327' 328' 329' 330' 331' 332' 333' 334' 335' 336' 337' 338' 339' 340' 341' 342' 343' 344' 345' 346' 347' 348' 349' 350' 351' 352' 353' 354' 355' 356' 357' 358' 359' 360' 361' 362' 363' 364' 365' 366' 367' 368' 369' 370' 371' 372' 373' 374' 375' 376' 377' 378' 379' 380' 381' 382' 383' 384' 385' 386' 387' 388' 389' 390' 391' 392' 393' 394' 395' 396' 397' 398' 399' 400' 401' 402' 403' 404' 405' 406' 407' 408' 409' 410' 411' 412' 413' 414' 415' 416' 417' 418' 419' 420' 421' 422' 423' 424' 425' 426' 427' 428' 429' 430' 431' 432' 433' 434' 435' 436' 437' 438' 439' 440' 441' 442' 443' 444' 445' 446' 447' 448' 449' 450' 451' 452' 453' 454' 455' 456' 457' 458' 459' 460' 461' 462' 463' 464' 465' 466' 467' 468' 469' 470' 471' 472' 473' 474' 475' 476' 477' 478' 479' 480' 481' 482' 483' 484' 485' 486' 487' 488' 489' 490' 491' 492' 493' 494' 495' 496' 497' 498' 499' 500' 501' 502' 503' 504' 505' 506' 507' 508' 509' 510' 511' 512' 513' 514' 515' 516' 517' 518' 519' 520' 521' 522' 523' 524' 525' 526' 527' 528' 529' 530' 531' 532' 533' 534' 535' 536' 537' 538' 539' 540' 541' 542' 543' 544' 545' 546' 547' 548' 549' 550' 551' 552' 553' 554' 555' 556' 557' 558' 559' 560' 561' 562' 563' 564' 565' 566' 567' 568' 569' 570' 571' 572' 573' 574' 575' 576' 577' 578' 579' 580' 581' 582' 583' 584' 585' 586' 587' 588' 589' 590' 591' 592' 593' 594' 595' 596' 597' 598' 599' 600' 601' 602' 603' 604' 605' 606' 607' 608' 609' 610' 611' 612' 613' 614' 615' 616' 617' 618' 619' 620' 621' 622' 623' 624' 625' 626' 627' 628' 629' 630' 631' 632' 633' 634' 635' 636' 637' 638' 639' 640' 641' 642' 643' 644' 645' 646' 647' 648' 649' 650' 651' 652' 653' 654' 655' 656' 657' 658' 659' 660' 661' 662' 663' 664' 665' 666' 667' 668' 669' 670' 671' 672' 673' 674' 675' 676' 677' 678' 679' 680' 681' 682' 683' 684' 685' 686' 687' 688' 689' 690' 691' 692' 693' 694' 695' 696' 697' 698' 699' 700' 701' 702' 703' 704' 705' 706' 707' 708' 709' 710' 711' 712' 713' 714' 715' 716' 717' 718' 719' 720' 721' 722' 723' 724' 725' 726' 727' 728' 729' 730' 731' 732' 733' 734' 735' 736' 737' 738' 739' 740' 741' 742' 743' 744' 745' 746' 747' 748' 749' 750' 751' 752' 753' 754' 755' 756' 757' 758' 759' 760' 761' 762' 763' 764' 765' 766' 767' 768' 769' 770' 771' 772' 773' 774' 775' 776' 777' 778' 779' 780' 781' 782' 783' 784' 785' 786' 787' 788' 789' 790' 791' 792' 793' 794' 795' 796' 797' 798' 799' 800' 801' 802' 803' 804' 805' 806' 807' 808' 809' 810' 811' 812' 813' 814' 815' 816' 817' 818' 819' 820' 821' 822' 823' 824' 825' 826' 827' 828' 829' 830' 831' 832' 833' 834' 835' 836' 837' 838' 839' 840' 841' 842' 843' 844' 845' 846' 847' 848' 849' 850' 851' 852' 853' 854' 855' 856' 857' 858' 859' 860' 861' 862' 863' 864' 865' 866' 867' 868' 869' 870' 871' 872' 873' 874' 875' 876' 877' 878' 879' 880' 881' 882' 883' 884' 885' 886' 887' 888' 889' 890' 891' 892' 893' 894' 895' 896' 897' 898' 899' 900' 901' 902' 903' 904' 905' 906' 907' 908' 909' 910' 911' 912' 913' 914' 915' 916' 917' 918' 919' 920' 921' 922' 923' 924' 925' 926' 927' 928' 929' 930' 931' 932' 933' 934' 935' 936' 937' 938' 939' 940' 941' 942' 943' 944' 945' 946' 947' 948' 949' 950' 951' 952' 953' 954' 955' 956' 957' 958' 959' 960' 961' 962' 963' 964' 965' 966' 967' 968' 969' 970' 971' 972' 973' 974' 975' 976' 977' 978' 979' 980' 981' 982' 983' 984' 985' 986' 987' 988' 989' 990' 991' 992' 993' 994' 995' 996' 997' 998' 999' 1000' 1001' 1002' 1003' 1004' 1005' 1006' 1007' 1008' 1009' 1010' 1011' 1012' 1013' 1014' 1015' 1016' 1017' 1018' 1019' 1020' 1021' 1022' 1023' 1024' 1025' 1026' 1027' 1028' 1029' 1030' 1031' 1032' 1033' 1034' 1035' 1036' 1037' 1038' 1039' 1040' 1041' 1042' 1043' 1044' 1045' 1046' 1047' 1048' 1049' 1050' 1051' 1052' 1053' 1054' 1055' 1056' 1057' 1058' 1059' 1060' 1061' 1062' 1063' 1064' 1065' 1066' 1067' 1068' 1069' 1070' 1071' 1072' 1073' 1074' 1075' 1076' 1077' 1078' 1079' 1080' 1081' 1082' 1083' 1084' 1085' 1086' 1087' 1088' 1089' 1090' 1091' 1092' 1093' 1094' 1095' 1096' 1097' 1098' 1099' 1100' 1101' 1102' 1103' 1104' 1105' 1106' 1107' 1108' 1109' 1110' 1111' 1112' 1113' 1114' 1115' 1116' 1117' 1118' 1119' 1120' 1121' 1122' 1123' 1124' 1125' 1126' 1127' 1128' 1129' 1130' 1131' 1132' 1133' 1134' 1135' 1136' 1137' 1138' 1139' 1140' 1141' 1142' 1143' 1144' 1145' 1146' 1147' 1148' 1149' 1150' 1151' 1152' 1153' 1154' 1155' 1156' 1157' 1158' 1159' 1160' 1161' 1162' 1163' 1164' 1165' 1166' 1167' 1168' 1169' 1170' 1171' 1172' 1173' 1174' 1175' 1176' 1177' 1178' 1179' 1180' 1181' 1182' 1183' 1184' 1185' 1186' 1187' 1188' 1189' 1190' 1191' 1192' 1193' 1194' 1195' 1196' 1197' 1198' 1199' 1200' 1201' 1202' 1203' 1204' 1205' 1206' 1207' 1208' 1209' 1210' 1211' 1212' 1213' 1214' 1215' 1216' 1217' 1218' 1219' 1220' 1221' 1222' 1223' 1224' 1225' 1226' 1227' 1228' 1229' 1230' 1231' 1232' 1233' 1234' 1235' 1236' 1237' 1238' 1239' 1240' 1241' 1242' 1243' 1244' 1245' 1246' 1247' 1248' 1249' 1250' 1251' 1252' 1253' 1254' 1255' 1256' 1257' 1258' 1259' 1260' 1261' 1262' 1263' 1264' 1265' 1266' 1267' 1268' 1269' 1270' 1271' 1272' 1273' 1274' 1275' 1276' 1277' 1278' 1279' 1280' 1281' 1282' 1283' 1284' 1285' 1286' 1287' 1288' 1289' 1290' 1291' 1292' 1293' 1294' 1295' 1296' 1297' 1298' 1299' 1300' 1301' 1302' 1303' 1304' 1305' 1306' 1307' 1308' 1309' 1310' 1311' 1312' 1313' 1314' 1315' 1316' 1317' 1318' 1319' 1320' 1321' 1322' 1323' 1324' 1325' 1326' 1327' 1328' 1329' 1330' 1331' 1332' 1333' 1334' 1335' 1336' 1337' 1338' 1339' 1340' 1341' 1342' 1343' 1344' 1345' 1346' 1347' 1348' 1349' 1350' 1351' 1352' 1353' 1354' 1355' 1356' 1357' 1358' 1359' 1360' 1361' 1362' 1363' 1364' 1365' 1366' 1367' 1368' 1369' 1370' 1371' 1372' 1373' 1374' 1375' 1376' 1377' 1378' 1379' 1380' 1381' 1382' 1383' 1384' 1385' 1386' 1387' 1388' 1389' 1390' 1391' 1392' 1393' 1394' 1395' 1396' 1397' 1398' 1399' 1400' 1401' 1402' 1403' 1404' 1405' 1406' 1407' 1408' 1409' 1410' 1411' 1412' 1413' 1414' 1415' 1416' 1417' 1418' 1419' 1420' 1421' 1422' 1423' 1424' 1425' 1426' 1427' 1428' 1429' 1430' 1431' 1432' 1433' 1434' 1435' 1436' 1437' 1438' 1439' 1440' 1441' 1442' 1443' 1444' 1445' 1446' 1447' 1448' 1449' 1450' 1451' 1452' 1453' 1454' 1455' 1456' 1457' 1458' 1459' 1460' 1461' 1462' 1463' 1464' 1465' 1466' 1467' 1468' 1469' 1470' 1471' 1472' 1473' 1474' 1475' 1476' 1477' 1478' 1479' 1480' 1481' 1482' 1483' 1484' 1485' 1486' 1487' 1488' 1489' 1490' 1491' 1492' 1493' 1494' 1495' 1496' 1497' 1498' 1499' 1500' 1501' 1502' 1503' 1504' 1505' 1506' 1507' 1508' 1509' 1510' 1511' 1512' 1513' 1514' 1515' 1516' 1517' 1518' 1519' 1520' 1521' 1522' 1523' 1524' 1525' 1526' 1527' 1528' 1529' 1530' 1531' 1532' 1533' 1534' 1535' 1536' 1537' 1538' 1539' 1540' 1541' 1542' 1543' 1544' 1545' 1546' 1547' 1548' 1549' 1550' 1551' 1552' 1553' 1554' 1555' 1556' 1557' 1558' 1559' 1560' 1561' 1562' 1563' 1564' 1565' 1566' 1567' 1568' 1569' 1570' 1571' 1572' 1573' 1574' 1575' 1576' 1577' 1578' 1579' 1580' 1581' 1582' 1583' 1584' 1585' 1586' 1587' 1588' 1589' 1590' 1591' 1592' 1593' 1594' 1595' 1596' 1597' 1598' 1599' 1600' 1601' 1602' 1603' 1604' 1605' 1606' 1607' 1608' 1609' 1610' 1611' 1612' 1613' 1614' 1615' 1616' 1617' 1618' 1619' 1620' 1621' 1622' 1623' 1624' 1625' 1626' 1627' 1628' 1629' 1630' 1631' 1632' 1633' 1634' 1635' 1636' 1637' 1638' 1639' 1640' 1641' 1642' 1643' 1644' 1645' 1646' 1647' 1648' 1649' 1650' 1651' 1652' 1653' 1654' 1655' 1656' 1657' 1658' 1659' 1660' 1661' 1662' 1663' 1664' 1665' 1666' 1667' 1668' 1669' 1670' 1671' 1672' 1673' 1674' 1675' 1676' 1677' 1678' 1679' 1680' 1681' 1682' 1683' 1684' 1685' 1686' 1687' 1688' 1689' 1690' 1691' 1692' 1693' 1694' 1695' 1696' 1697' 1698' 1699' 1700' 1701' 1702' 1703' 1704' 1705' 1706' 1707' 1708' 1709' 1710' 1711' 1712' 1713' 1714' 1715' 1716' 1717' 1718' 1719' 1720' 1721' 1722' 1723' 1724' 1725' 1726' 1727' 1728' 1729' 1730' 1731' 1732' 1733' 1734' 1735' 1736' 1737' 1738' 1739' 1740' 1741' 1742' 1743' 1744' 1745' 1746' 1747' 1748' 1749' 1750' 1751' 1752' 1753' 1754' 1755' 1756' 1757' 1758' 1759' 1760' 1761' 1762' 1763' 1764' 1765' 1766' 1767' 1768' 1769' 1770' 1771' 1772' 1773' 1774' 1775' 1776' 1777' 1778' 1779' 1780' 1781' 1782' 1783' 1784' 1785' 1786' 1787' 1788' 1789' 1790' 1791' 1792' 1793' 1794' 1795' 1796' 1797' 1798' 1799' 1800' 1801' 1802' 1803' 1804' 1805' 1806' 1807' 1808' 1809' 1810' 1811' 1812' 1813' 1814' 1815' 1816' 1817' 1818' 1819' 1820' 1821' 1822' 1823' 1824' 1825' 1826' 1827' 1828' 1829' 1830' 1831' 1832' 1833' 1834' 1835' 1836' 1837' 1838' 1839' 1840' 1841' 1842' 1843' 1844' 1845' 1846' 1847' 1848' 1849' 1850' 1851' 1852' 1853' 1854' 1855' 1856' 1857' 1858' 1859' 1860' 1861' 1862' 1863' 1864' 1865' 1866' 1867' 1868' 1869' 1870' 1871' 1872' 1873' 1874' 1875' 1876' 1877' 1878' 1879' 1880' 1881' 1882' 1883' 1884' 1885' 1886' 1887' 1888' 1889' 1890' 1891' 1892' 1893' 1894' 1895' 1896' 1897' 1898' 1899' 1900' 1901' 1902' 1903' 1904' 1905' 1906' 1907' 1908' 1909' 1910' 1911' 1912' 1913' 1914' 1915' 1916' 1917' 1918' 1919' 1920' 1921' 1922' 1923' 1924' 1925' 1926' 1927' 1928' 1929' 1930' 1931' 1932' 1933' 1934' 1935' 1936' 1937' 1938' 1939' 1940' 1941' 1942' 1943' 1944' 1945' 1946' 1947' 1948' 1949' 1950' 1951' 1952' 1953' 1954' 1955' 1956' 1957' 1958' 1959' 1960' 1961' 1962' 1963' 1964' 1965' 1966' 1967' 1968' 1969' 1970' 1971' 1972' 1973' 1974' 1975' 1976' 1977' 1978' 1979' 1980' 1981' 1982' 1983' 1984' 1985' 1986' 1987' 1988' 1989' 1990' 1991' 1992' 1993' 1994' 1995' 1996' 1997' 1998' 1999' 2000' 2001' 2002' 2003' 2004' 2005' 2006' 2007' 2008' 2009' 2010' 2011' 2012' 2013' 2014' 2015' 2016' 2017' 2018' 2019' 2020' 2021' 2022' 2023' 2024' 2025' 2026' 2027' 2028' 2029' 2030' 2031' 2032' 2033' 2034' 2035' 2036' 2037' 2038' 2039' 2040' 2041' 2042' 2043' 2044' 2045' 2046' 2047' 2048' 2049' 2050' 2051' 2052' 2053' 2054' 2055' 2056' 2057' 2058' 2059' 2060' 2061' 2062' 2063' 2064' 2065' 2066' 2067' 2068' 2069' 2070' 2071' 2072' 2073' 2074' 2075' 2076' 2077' 2078' 2079' 2080' 2081' 2082' 2083' 2084' 2085' 2086' 2087' 2088' 2089' 2090' 2091' 2092' 2093' 2094' 2095' 2096' 2097' 2098' 2099' 2100' 2101' 2102' 2103' 2104' 2105' 2106' 2107' 2108' 2109' 2110' 2111' 2112' 2113' 2114' 211

Claim 17, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Claim 23, line 1, delete "21 or"

Claim 24, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Claim 28, lines 2-3, change "any one of Claims 24 to 27" to --Claim 24--.

Claim 29, line 2, change "Claims 1 to 11" to --Claims 3 to 9 and 11--.

Please add the following new claims:

*Sub G3*  
--31. The method of Claim 30, wherein said motor neuron disorder is spinal muscular atrophy.--

*B, Sub #3*  
--32. The method of Claim 30, wherein steps (c) and (d) are replaced with a step of digestion with a Bsrl enzyme.--

*Sub G4*  
--33. A method for detecting spinal muscular atrophy said method comprising the steps of:

(a) extracting DNA from a patient sample;

cm  
G4  
(b) hybridizing said DNA with a DNA probe comprising all or part of the DNA sequence of Figure 3 under stringent conditions; and

(c) detecting the hybrids possibly formed.--

--34. The method according to Claim 33, wherein said probe is radiolabeled.--

B4 cm+  
--35. A monoclonal antibody or a polyclonal antiserum directed against the SMN protein of Figure 1, or against the protein of Figure 8, or against the protein of Figure 12.--

Sub G4  
--36. A method for detecting arthrogryposis multiplex congenita (AMC), said method comprising the steps of:

- (a) extracting DNA from a patient sample;  
(b) amplifying said DNA via PCR using unlabeled primers from exon 7 and exon 8 of the SMN gene;  
(c) subjecting said amplified DNA to SCCP;  
(d) autoradiographing the gels; and  
(e) detecting the presence or absence of arthrogryposis multiplex congenita.--

--37. An isolated nucleotide sequence of Figure 11.--

--38. A transgenic mouse that only expresses the human SMN protein of Figure 1.--

--39. A transgenic mouse that expresses a mutated SMN protein of Figure 1.--

--40. A method of detecting the presence in a human patient of an altered SMN gene associated with spinal muscular atrophy, comprising

analyzing exon 7 or exon 8 of a gene identified as T-BCD541 in a biological sample derived from the patient, and

comparing said exon to the corresponding exon derived from T-BCD541 from normal human tissue;

wherein an alteration of either exon 7 or exon 8 in said patient sample with reference to said normal tissue is indicative of the presence of an altered SMN gene associated with spinal muscular atrophy in said patient.--

--41. The method of claim 40, wherein said analyzing comprises

determining whether T-BCD541 exon 7 is present or absent in the patient sample.--

--42. The method of claim 40, wherein said analyzing comprises

determining whether T-BCD541 exon 8 is present or absent in the patient sample.--

*Sw H6*  
--43. The method of either of claim 40, wherein said analyzing includes amplifying all or part of the T-BCD541 gene.--

--44. The method of claim 43, wherein said analyzing comprises

amplifying a nucleotide fragment from said patient sample comprising exon 7 of the T-BCD541 gene,

*cont*  
amplifying a nucleotide fragment from said patient sample comprising exon 8 of the T-BCD541 gene, and

*B4*  
determining whether said exon 7 and said exon 8 are present or absent in said amplified fragments.--

*Sw H6*  
--45. The method of claim 44, wherein said determining includes

subjecting said exon 7 comprising nucleotide fragment to restriction enzyme digestion,

subjecting said exon 8 comprising nucleotide fragment to restriction enzyme digestion, and

analyzing enzymatic digestion products produced by said enzymatic digestions,

wherein an alteration of either exon 7 or exon 8 with reference to normal tissue is evidenced by an altered restriction enzymatic digestion pattern in one or both of said exons.--

--46. The method of claim 43, wherein said amplifying is carried out using a polymerase chain reaction using a primer





--51. The method of claim 50, wherein said analyzing comprises

amplifying a nucleotide fragment from said patient sample comprising exon 7 of the T-BCD541 gene,

amplifying a nucleotide fragment of said patient sample comprising exon 8 of the T-BCD541 gene, and

determining whether said exon 7 and said exon 8 are present or absent in said amplified nucleotide fragments.--

--52. The method of claim 51, wherein said determining includes

subjecting said exon 7 comprising nucleotide fragment to restriction enzyme digestion,

subjecting said exon 8 comprising nucleotide fragment to restriction enzyme digestion, and

analyzing enzymatic digestion products produced by said enzymatic digestions,

wherein an alteration of either exon 7 or exon 8 with reference to normal tissue is evidenced by an altered restriction enzymatic digestion pattern in one or both of said exons.--

#### REMARKS

Enclosed herewith in full compliance with 37 C.F.R. §1.821-1.825 is a Substitute Sequence Listing to be inserted into the